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Review

Salmonella Senftenberg: A Highly Adaptable Serovar Across Poultry Production and the Food Chain

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Abstract

Salmonella enterica subspecies *enterica* serovar Senftenberg comprises a heterogeneous group of nontyphoidal *Salmonella* strains frequently detected in animal feed, feed ingredients, feed-manufacturing facilities, poultry production, and a wide range of foods. Genomic analyses indicate that *S.* Senftenberg is polyphyletic, comprising multiple genetically distinct evolutionary lineages and considerable phenotypic variation among isolates. Certain strains exhibit remarkable tolerance to heat, desiccation, and routine cleaning and disinfection procedures, facilitating their persistence in these environments and potentially contributing to transmission through the food chain. Human infections associated with *S.* Senftenberg range from self-limiting gastroenteritis to invasive disease, while some outbreak-associated isolates have demonstrated resistance to antimicrobials of particular importance in human medicine, adaptation to plant-derived antimicrobial compounds, and unusual virulence profiles. This review examines *S.* Senftenberg as an example of how adaptive traits can contribute to the persistence of *Salmonella* under environmental and selective pressures, with emphasis on its occurrence and persistence in poultry production and implications for food safety and public health.

Keywords: *Salmonella* Senftenberg; poultry production; persistence; stress tolerance; genetic diversity; antimicrobial resistance; human outbreaks

1. Introduction

The genus *Salmonella* currently comprises two recognized species, *Salmonella enterica* and *Salmonella bongori*, although genomic studies continue to refine its taxonomy. *S. enterica* comprises at least 6 subspecies designated by Roman names and numerals: *enterica* (I), *salamae* (II), *arizonae* (IIIa), *diarizonae* (IIIb), *houtenae* (IV), and *indica* (VI). Recent genomic surveys of large collections of isolates indicate that *S. enterica* may contain up to five additional subspecies, while *Salmonella subterranea* may be considered a third *Salmonella* species [1]. Whole-genome sequencing (WGS) is increasingly used for *Salmonella* serotyping and classification. In addition to accurate serovar identification, WGS enables high-resolution outbreak investigation, source attribution, surveillance of emerging clones, characterization of atypical strains and the identification of novel or antimicrobial-resistant variants, making it an indispensable tool for modern public health and food-safety surveillance [2–4].

According to the White–Kauffman–Le Minor classification scheme, the genus is further subdivided into more than 2600 serovars based on their somatic (O) and flagellar (H) antigens. The subspecies *enterica* includes approximately 1600 serovars. From a clinical perspective, serovars of the *Salmonella enterica* subspecies *enterica* are broadly classified

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as typhoidal or nontyphoidal *Salmonella* (NTS). Unlike typhoidal serovars, which are human-restricted pathogens causing enteric fever, NTS serovars are zoonotic agents that predominantly cause gastroenteritis but may also lead to invasive infections, particularly in vulnerable individuals [3]. Twelve Salmonella serovars, including *S.* Enteritidis, *S.* Typhimurium, and monophasic *S.* Typhimurium, account for approximately 90% of reported foodborne outbreaks [5]. Globally, NTS is estimated to cause between 200 million and one billion infections annually, including more than 90 million cases of gastroenteritis and over 150,000 deaths, with approximately 85% of infections associated with the consumption of contaminated food [3,6,7]. Accordingly, human salmonellosis remains one of the leading foodborne diseases worldwide, and its incidence has shown no sustained decline in recent years [5,8].

Salmonella enterica subspecies *enterica* serovar Senftenberg (*S.* Senftenberg) (antigenic formula 1,3,19:g,[s],t:-) has received comparatively less attention than serovars most frequently associated with human infections worldwide, such as *S.* Typhimurium and *S.* Enteritidis [9]. Nevertheless, *S.* Senftenberg has been repeatedly detected in animal feed, feed ingredients, feed manufacturing facilities, poultry farms, and a wide variety of foods, including fennel seed tea, nuts, herbs, infant cereals, poultry meat, and spices [8,10,11].

S. Senftenberg is a polyphyletic serovar whose isolates have been assigned to different sequence types (STs) [12]. Whole-genome sequencing studies have shown that *S.* Senftenberg comprises at least two major genetically distinct lineages, represented by ST14 and ST185 [10,11]. Phylogenetic analyses further classified *S.* Senftenberg isolates into two major clades, designated Senftenberg clades 1 (SC1) and 2 (SC2); SC1 comprises ST185, ST217, and ST1751, whereas SC2 includes ST14 [12]. ST14 is a common and globally distributed lineage that lacks apparent host specificity and has been associated with humans, animals, food, and food production environments. Considerable diversity among ST14 isolates has also been demonstrated by pulsed-field gel electrophoresis (PFGE), which revealed multiple distinct profiles within the serovar [10]. Such genetic diversity may contribute to the phenotypic variability observed among *S.* Senftenberg isolates.

While previous reviews have broadly addressed *Salmonella* persistence and control in poultry production, a serovar-specific synthesis integrating the genetic diversity of *S.* Senftenberg with its phenotypic and adaptive traits is lacking. This perspective is particularly relevant for *S.* Senftenberg because genetically distinct lineages and considerable strain-level variation may underlie differences in environmental persistence, stress tolerance, and responses to control measures.

Certain strains of this serovar exhibit remarkable tolerance to heat, desiccation, and routine cleaning and disinfection procedures. These characteristics can facilitate long-term persistence in poultry production environments and increase the potential for transmission through the food chain [13–15]. In humans, *S.* Senftenberg has been implicated in foodborne outbreaks and healthcare-associated infections worldwide [16–32].

Accordingly, this review synthesizes epidemiological, ecological, phenotypic, and genomic evidence on *S.* Senftenberg, with particular emphasis on its occurrence and persistence in poultry production, environmental reservoirs, stress tolerance, antimicrobial resistance, and implication for food safety and public health.

2. Occurrence of *S.* Senftenberg in Poultry Production

Poultry meat, eggs, and egg products continue to represent some of the major sources of human salmonellosis despite decades of intensive surveillance and control programs aimed at reducing the prevalence of *Salmonella* in poultry production [7,8,33–35]. Although *Salmonella* can enter the food chain at any stage of production, effective control at the farm level is considered essential for reducing contamination during subsequent processing [8].

Within the European Union, National Control Programs (NCPs) have substantially improved the monitoring and control of the serovars considered to pose the greatest public health risk: *S.* Enteritidis, *S.* Typhimurium, monophasic variant of *S.* Typhimurium, and the additional target serovars *S.* Hadar, *S.* Infantis, and *S.* Virchow [8,36,37]. A comparative analysis of European surveillance and control programs conducted between 2017 and 2021 included data on all *Salmonella* serovars in poultry production. *S.* Senftenberg was one of the most frequently detected serovars in broiler farms in Denmark in 2018 and in Italy in both 2019 and 2021. It was among the five most frequently isolated serovars from fattening turkeys in Italy in 2018, in France in 2019 and in Germany in 2020 [8]. Likewise, surveillance conducted in the Belgrade epizootiological area in Serbia identified *S.* Senftenberg among the five most frequently detected *Salmonella* serovars in poultry between 2014 and 2019 [38]. In the USA, *S.* Senftenberg is among the top five serovars isolated from food and the top 11 serovars isolated from clinically ill animals [11]. In recent decades, *S.* Senftenberg has also been detected at multiple stages of the poultry production chain, including broiler farms, poultry environments, slaughterhouses, and chicken carcasses in Brazil [39].

These findings support the need for periodic revision of National Control Programs to reflect changing epidemiological patterns [36]. The prevalence and distribution of *Salmonella* serovars may vary considerably across locations, regions, and countries; therefore, continuous surveillance in both humans and poultry is essential to identify prevalent serovars and to guide evidence-based control strategies [14]. In addition to prevalence in poultry flocks and public health relevance, antimicrobial resistance, virulence characteristics, and the potential for rapid spread should also be considered when evaluating serovars of increasing epidemiological importance for inclusion in future surveillance and control programs [8,40].

2.1. Persistence of S. Senftenberg in Poultry Farms

Contaminated feed and feed ingredients are considered major routes by which *S.* Senftenberg may be introduced into commercial poultry production. This serovar was frequently detected in animal feed, feed ingredients, feed manufacturing plants, and on-farm feed environments [41–43]. A global systematic review and meta-analysis further highlighted the close association of *S.* Senftenberg with the feed production chain. *S.* Senftenberg was the most frequently reported serovar among *Salmonella* isolates from finished feed and from feed mill equipment and feed mill environment, with reports from Europe, the Americas, and the Western Pacific [44]. It also ranked second among isolates across all sample types, including finished feed, raw feed components, feed mill equipment, and feed mill environment and was detected in all seven regions included in the analysis [44]. Persistent contamination of a Swedish feed mill during 1995–1996 demonstrated the ability of *S.* Senftenberg to establish long-term reservoirs within feed manufacturing facilities. Molecular typing identified the contamination source, and targeted control measures subsequently eliminated the persistent clone [45]. Evidence from Japan demonstrated that contaminated feed may introduce a single clone into poultry farms, followed by its dissemination through the farm environment [14]. More recently, repeated isolation of *S.* Senftenberg from the same feed-processing enterprise in Ukraine over a two-year period further confirmed that feed manufacturing facilities may act as long-term reservoirs of this serovar [43].

Once introduced into poultry production, *S.* Senftenberg may become established in multiple reservoirs within the production environment, including hatcheries, dust, litter, feed, and poultry house equipment. One of the earliest reports showed that *S.* Senftenberg was able to survive and multiply in hatchery incubators under normal temperature and humidity conditions throughout the hatching process [46]. Once present in the hatchery, contamination spread through airborne transmission, as well as via contaminated hands

and equipment handled by hatchery personnel. Although the original source of contamination could not be confirmed, the authors considered several potential sources, including contaminated eggs, rodents, wild birds, flies and feed. A subsequent report described an ST14 strain isolated from a hatchery and associated with long-term intestinal colonization of broiler chickens, further demonstrating the ability of *S.* Senftenberg to become established in poultry [47]. The multiple routes of introduction and environmental reservoirs that may contribute to its establishment and persistence in poultry production are summarized in Figure 1.

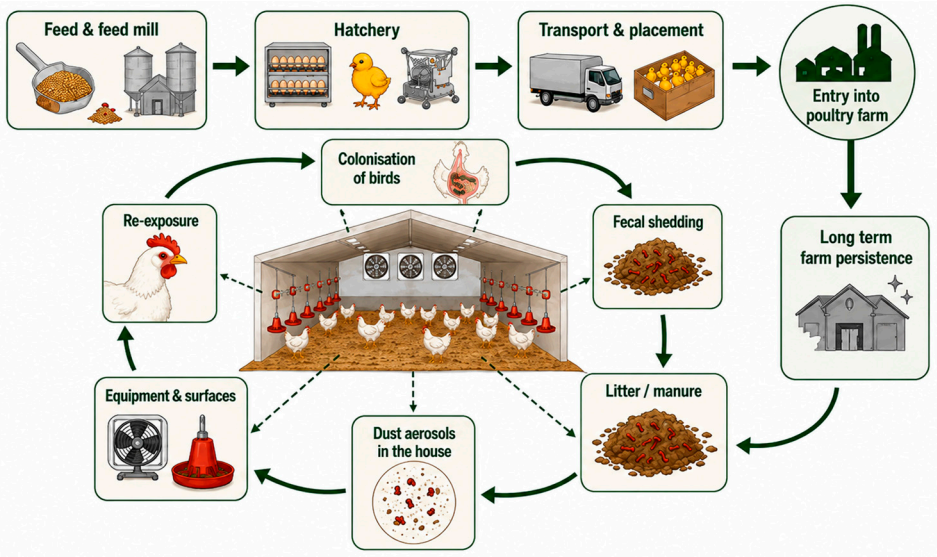

Figure 1. *S.* Senftenberg: multiple routes of entry-multiple reservoirs-long term persistence within the poultry production environment.

Long-term maintenance within poultry farms is illustrated particularly well by observations from broiler stock farms. On one farm, three isolates of *S.* Senftenberg collected over a 30-month period had identical pulsed-field gel electrophoresis (PFGE) profiles, indicating the persistence of a single clone despite depopulation, cleaning, and disinfection procedures [13]. The strain was subsequently able to infect *Salmonella*-free layer chickens. Moreover, on another farm, genetically identical isolates were recovered from the poultry house despite 55 consecutive negative *Salmonella* test results over an 18-month interval between positive sampling events. PFGE analysis further suggested that isolates recovered from the farms were genetically related to isolates obtained from feed raw materials, indicating that contaminated feed ingredients and feed mill environments may contribute to the introduction and long-term maintenance of *S.* Senftenberg in poultry production systems [13].

The remarkable tolerance of *S.* Senftenberg to desiccation may further facilitate its survival in dust, litter, and on poultry house equipment. This tolerance may also complicate environmental monitoring, as dormant or low-level *Salmonella* cells can remain in dust, dry fecal material, and on contaminated surfaces or equipment after cleaning and disinfection, potentially escaping routine hygiene checks [33]. Contaminated dust may facilitate airborne transmission of *S.* Senftenberg within poultry flocks. Experimental studies demonstrated that intratracheal inoculation of 7-day-old chicks resulted in successful cecal colonization, whereas oral and intravenous inoculation with the same field strain did not [48].

In addition to desiccation tolerance, biofilm formation represents another mechanism promoting environmental survival. Like many other *Salmonella* serovars, *S.* Senftenberg is capable of forming biofilms that protect bacterial cells from cleaning and disinfection procedures, thereby facilitating their survival in poultry production environments [43,49,50].

Environmental persistence is further complemented by the ability of some *S.* Senftenberg strains to establish prolonged colonization in poultry. In contrast to earlier observations that *S.* Senftenberg disappeared from chicks within 4–6 weeks under good husbandry conditions [46], subsequent studies revealed considerable strain-to-strain variation in colonization ability. Certain strains are able to colonize the ceca of chickens at high levels, similar to *S.* Enteritidis, establishing long-term asymptomatic infection without detectable antibody production [15,51]. Asymptomatic carrier birds can shed these strains of *S.* Senftenberg into the environment over prolonged periods, providing an additional mechanism for maintaining contamination within poultry flocks. In addition, the survival of *S.* Senftenberg in poultry litter applied as an organic fertilizer may contribute to contamination of agricultural soils, crops or recycled bedding material, thereby extending opportunities for transmission along the food chain [52].

The persistence of *Salmonella* in poultry environments and the difficulty of eliminating resident strains underscore the need for more sustainable and effective control strategies. Such resident *Salmonella* serovars may persist for years despite conventional hygiene measures [53]. Consequently, a range of alternative or complementary approaches is being investigated, including chemical, physical, and biological treatments. These include nanoparticles, ultraviolet light, heat, pressurized steam, infrared radiation, bacteriophages, essential oils, and other biofilm-targeting approaches [54].

2.2. Implications for Food Safety and Public Health

Persistent *S.* Senftenberg strains may represent an important food safety concern because they can colonize the intestinal tract, survive throughout the poultry production cycle, and remain present at slaughter and during food processing, potentially entering the food chain and causing human infection [15]. These observations emphasize that persistence may contribute substantially to the public health significance of this serovar. This risk may be further increased by the exceptional heat resistance exhibited by certain *S.* Senftenberg strains, which is of particular importance for food safety.

One of the earliest investigations identified an *S.* Senftenberg strain isolated from home-slaughtered meat in England with an F_{140} value of 39 min, i.e., a measure of thermal resistance at 140 °F (60 °C). This value was approximately ten times higher than the F_{140} value reported for *S.* Typhimurium (3–5 min), highlighting the exceptional thermotolerance of this *S.* Senftenberg strain [55]. Subsequent studies established *S.* Senftenberg strain ATCC 43845 (NCTC 9959), originally referred to as strain 775W, as a well-characterized model of exceptional thermotolerance. The strain was isolated in 1941 from Chinese egg powder in the United States and first reported as exceptionally heat-resistant in 1946 [56,57]. Among approximately 300 cultures of *Salmonella*, representing 75 different serotypes, none was found to be as heat-resistant as *S.* Senftenberg 775W [56].

Unlike most frequently encountered *Salmonella* serovars *S.* Enteritidis and *S.* Typhimurium, *S.* Senftenberg 775W exhibits exceptional resistance to conventional liquid egg pasteurization conditions. Based on published heat-resistance data, pasteurization at 60 °C for 3.5 min or 64 °C for 2.5 min would be expected to achieve only a 1–4 log reduction in *S.* Senftenberg 775W, compared with an estimated 5–9 log reduction for *S.* Enteritidis and *S.* Typhimurium [58]. Genomic analyses revealed that its exceptional thermotolerance is associated with two horizontally acquired thermotolerance loci, TLPQC-1 and TLPQC-2, located on a large IncHI2 plasmid [57]. Their presence may reflect adaptation to heat stress encountered during egg processing, although the evolutionary origin of these loci remains uncertain. The exceptional thermotolerance of certain *S.* Senftenberg strains illustrates how horizontally acquired genetic traits may compromise the effectiveness of conventional food-processing strategies.

3. Human Infections and Outbreaks Associated with *S.* Senftenberg

Although *S.* Senftenberg is not among the *Salmonella* serovars most frequently associated with human infection worldwide, it has been implicated in a wide range of sporadic infections, foodborne outbreaks, and occasional invasive disease [9,22]. Human infections are most commonly associated with consumption of contaminated foods, although several healthcare-associated outbreaks, particularly in neonatal units, have also been reported. Clinical manifestations range from asymptomatic carriage and self-limiting gastroenteritis to severe invasive infections. Table 1 summarizes available published reports of human infections and outbreaks associated with *S.* Senftenberg, arranged chronologically to illustrate the diversity of infection sources, clinical presentations, and epidemiological settings.

Table 1. Available published reports of human infections and outbreaks associated with *S.* Senftenberg.

Year	Country	Event	No. of Cases	Source of Infection	Key Findings and ST/Lineage *	References
1963–1965	United Kingdom	Hospital outbreak	NR	Turkey meat	Linked to contaminated fish meal used in turkey feed; ST/lineage: NR	[16]
1976	United Kingdom	Foodborne outbreak	More than 200 confirmed cases among children and teachers, and 60 food handlers	Sliced pork pies	Contaminated pork pies Large foodborne outbreak ST/lineage: NR	[17] **
NR *	India	Pediatric ward and nursery outbreak	7 patients and 7 asymptomatic carriers	Environmental contamination (intravenous stand, switchboard, electrical extension board)	All isolates were multidrug-resistant; ST/lineage: NR	[18]
1987–1988	India	Neonatal hospital outbreak	35 neonates (5 died)	Not identified	High mortality (14.3%) ST/lineage: NR	[19]
1990	India	Neonatal hospital outbreak	26 infants (22 neonates and 4 older infants)	Not identified	High mortality (19.2%) ST/lineage: NR	[20]
1992	India	Neonatal hospital outbreak	5 neonates (1 died)	Not identified	Invasive bloodstream infection ST/lineage: NR	[21]
1993–1994	United States	Hospital outbreak	22 confirmed cases; delayed detection; estimated >200 total infections	Contaminated turkey, secondary spread via kitchen equipment	Prolonged outbreak (21 months) ST/lineage: NR	[22]
1995	United Kingdom	Foodborne outbreak	Eight infants	Baby cereal	Outbreak strains lacked a plasmid compared with other contemporary human isolates of *S.* Senftenberg; ST/lineage: NR	[23]

Table 1. *Cont.*

Year	Country	Event	No. of Cases	Source of Infection	Key Findings and ST/Lineage *	References
1997–1998	United States	Foodborne outbreak	60 patients	Alfalfa clover mixed sprouts	Prolonged multistate sprout-associated outbreak; ST/lineage: NR	[24]
1999–2005	United States	Hospital outbreak	67 patients	Unknown source. Healthcare-associated transmission	First report of healthcare-associated fluoroquinolone-resistant strain; ST/lineage: NR	[25]
2002	China	Clinical outbreak	7 immunocompetent individuals	Not reported	Atypical variants of *S.* Senftenberg that lacked functional SPI-1 and portions of SPI-2; ST/lineage: ST217	[26]
2007	United Kingdom	Foodborne outbreak	55 human cases	Fresh basil	Adaptation to the plant-derived antimicrobial compound linalool: ST/lineage: NR	[27]
2007–2008	Serbia	Foodborne outbreak	14 (10 infants and 4 adults)	Baby tea with contaminated fennel seeds	First documented outbreak of salmonellosis linked to consumption of plant product in the province of Vojvodina, Serbia; ST/lineage: NR	[28]
2012	Zambia	Clinical cases	2 patients (1 died)	Unknown source	Extremely drug-resistant isolates of *S.* Senftenberg; ST/lineage: ST14	[29]
2013 and 2016	United States	Foodborne outbreak	10 clinical cases	Pistachios	Persistent *S.* Senftenberg strains carrying Copper Homeostasis and Silver Resistance Island (CHASRI) suggested adaptation to the pistachio supply chain; ST/lineage: ST185 (2013 outbreak); ST14 (2016 outbreak).	[30]
2022	United States	Foodborne outbreak	21 clinical cases (4 hospitalizations)	Peanut butter	Persistent environmental contamination in low-moisture processing facility; WGS linked the clinical isolates to a strain recovered from the facility in 2010; ST/lineage: NR	[31]

Table 1. *Cont.*

Year	Country	Event	No. of Cases	Source of Infection	Key Findings and ST/Lineage *	References
2023	13 countries EU/EEA	Foodborne outbreak	92 cases (1 death)	cherry-like tomatoes as the possible vehicle of infection	The majority of isolates were genetically similar, indicating a common source, ST/lineage: ST14	[32]

NR *: 1987. year of publication of the outbreak report; the year of occurrence was not specified in the original publication [18]; [17] **: Information obtained from the digitized scan available through the WHO IRIS repository: https://iris.who.int/server/api/core/bitstreams/c092138f-fce1-46ea-ae0e-d9f6a7b26b81/content (accessed on 31 August 2026); ST/lineage *: ST, sequence type; NR: not reported.

The reports summarized in Table 1 demonstrate the remarkable ecological and epidemiological versatility of *S.* Senftenberg, encompassing foodborne and healthcare-associated transmission, diverse food vehicles, prolonged environmental persistence, multidrug-resistant clones, and atypical virulence profiles. Collectively, these observations support the view that *S.* Senftenberg can adapt to diverse ecological niches and selective pressures, with implications for both food safety and public health.

In a study of 130 *S.* Senftenberg isolates recovered from humans, food, and environmental sources in Shanghai between 2005 and 2011, 56 PFGE profiles were identified, including four major profiles that showed high levels of genetic similarity (95.7%). The recovery of closely related isolates from food of an animal origin and environmental sources over a three-year period (2008–2010) suggested potential cross-contamination and possible persistent contamination by the same clone, highlighting the possible role of contaminated food and water as sources of human infection [59].

3.1. Unusual Characteristics of S. Senftenberg Isolates from Food and Human Outbreaks

3.1.1. Atypical Phenotypes and Challenges for Food Safety

In a recent study, an atypical strain of *S.* Senftenberg isolated from cooked mussels exhibited two features that may challenge conventional detection: absence of H_2S production and loss of detectable somatic antigen expression [4]. The H_2S-negative phenotype is relevant for culture-based surveillance because routine identification relies on characteristic colony morphology on selective media, including formation of black colonies on XLD agar [60]. Similar H_2S-negative variants were previously reported in China, including isolates belonging to the novel ST1751 and carrying a characteristic *phsA* mutation [61]. Conventional serotyping of the mussels isolate identified only the antigens of the first flagellar phase (-;g,s,t:-), whereas somatic antigens could not be detected. The loss of somatic antigen expression in this isolate was associated with a chromosomal rearrangement within the *rfb* operon, which encodes enzymes involved in O-antigen biosynthesis; variations within this cluster contribute to the diversity of somatic antigens observed across the *Salmonella* genus. Together, these findings illustrate the difficulties associated with reliable detection and identification of atypical *S.* Senftenberg variants in food safety surveillance using conventional phenotypic methods [4].

In silico serotyping and MLST analyses identified the isolate as *S.* Senftenberg (1,3,19:g,s,t:-), belonging to ST14. Interestingly, closely related *S.* Senftenberg ST14 strains have been repeatedly recovered from shellfish and shellfish-processing environments in Galicia, Spain, where this serovar has predominated for more than two decades. Whole-genome multi locus sequence typing (wgMLST) analysis showed that the recent atypical isolate was closely related to an ST14 strain recovered in 2015, and both shared an identical chromosomal rearrangement at the *rfb* operon, supporting the possibility of long-term

persistence and adaptation to this specific ecological niche. However, the limited number of currently available closely related isolates precludes definitive conclusions regarding the endemic persistence of this lineage [4].

3.1.2. Adaptation to Antimicrobial Compounds and Antimicrobial Resistance

Clinical isolates associated with the 2007 foodborne outbreak in England and Wales exhibited resistance to basil essential oil and its major compound, linalool, a naturally occurring terpene alcohol. Experimental exposure to increasing linalool concentrations resulted in an eightfold increase in linalool resistance and enhanced survival on basil plants before and after harvest. In addition, adapted isolates displayed cross-resistance to trimethoprim, sulfamethoxazole, piperacillin, chloramphenicol, and tetracycline, with MICs increasing 2- to 32-fold [62].

Although the complex, multicomponent composition and multiple cellular targets of essential oils may reduce the likelihood of bacterial resistance, experimental evidence indicates that adaptive responses may nevertheless develop following prolonged exposure to sublethal concentrations [62]. In *S.* Senftenberg, repeated exposure to linalool resulted in stable adaptation associated with increased tolerance to basil essential oil and reduced susceptibility to several antibiotics used in clinical and veterinary medicine. Tolerance to linalool involves multiple adaptive mechanisms, including chemotaxis-regulated motility, changes in membrane composition, induced efflux, reduced influx, and the formation of larger aggregates. Importantly, the adapted phenotype remained stable after repeated subculturing, indicating that the observed resistance was associated with genetic shift rather than epigenetic changes [62].

A striking example of clinically relevant antimicrobial resistance was reported during a prolonged healthcare-associated outbreak in northeast Florida in 1999. A multidrug-resistant strain of *S.* Senftenberg was isolated from a patient in a Jacksonville, Florida hospital, and over the next 6 years, it spread to 15 other healthcare institutions through repeated patient transfers, affecting a total of 67 patients [25]. Subsequent molecular characterization of the outbreak isolates revealed chromosomal mutations associated with decreased susceptibility to fluoroquinolones together with acquired β-lactam resistance genes conferring resistance to extended-spectrum cephalosporins, highlighting the capacity of this serovar to acquire and maintain clinically important antimicrobial resistance determinants under selective pressure [63]. Extremely drug-resistant strains of *S.* Senftenberg were also isolated from two patients in Zambia. The isolates were resistant to, and harbored genes conferring resistance to, nine antimicrobial classes, including fluoroquinolones and extended-spectrum cephalosporins [29].

Fluoroquinolone-resistant NTS and typhoidal *Salmonella* are currently classified by the World Health Organization (WHO) as "high-priority" pathogens, while ceftriaxone-resistant isolates have been increasingly reported across multiple countries and continents, underscoring the global scale of this challenge [3].

Antimicrobial use in food-producing animals is an important selective pressure that may contribute to the emergence and maintenance of antimicrobial-resistant *Salmonella* strains, which may subsequently enter the food chain. In a study of *S.* Senftenberg isolates from human and animal sources in the United States, antimicrobial resistance was detected only among animal isolates, suggesting that animal husbandry has a significant influence on the selection and promotion of antimicrobial resistance [10]. A subsequent study of *S.* Senftenberg isolates from food-producing animals found multidrug resistance in 39.4% of isolates, with a particularly high prevalence among isolates from swine (60%). Four isolates from swine exhibited extensive drug resistance to 12 or 13 antimicrobial agents. In addition, 25 MDR isolates carried the *qacEΔ1* gene, which is associated with reduced susceptibility to

quaternary ammonium compound disinfectants such as benzalkonium chloride [11]. The co-occurrence of antimicrobial and disinfectant resistance traits may further complicate the control of *S.* Senftenberg in food-producing animals.

3.1.3. Specific Virulence Potential of *S.* Senftenberg

Owing to the clinical importance of *Salmonella*, various serovars, especially *S.* Typhimurium, are frequently used as a model for studying invasiveness and host–pathogen interactions at the molecular level [64]. These studies identified numerous virulence determinants located on plasmids and within chromosomal pathogenicity islands, among which *Salmonella* Pathogenicity Islands 1 and 2 (SPI-1 and SPI-2) are considered the most important [35,65,66]. Both islands encode the components of type III secretion systems (T3SSs), virulence factors detected in various Gram-negative pathogens [64,66]. According to the prevailing model of *Salmonella* enteropathogenesis, SPI-1 is essential for invasion of the intestinal epithelium [67]. Conserved SPI-1 genes such as *invA* and *hilA* have long been used as molecular markers for the detection of enteropathogenic *S. enterica* and are important determinants of invasion of intestinal epithelial cells.

However, *S.* Senftenberg has challenged this paradigm. Two clinical isolates recovered during a foodborne outbreak in Shenzhen, China in 2002, lacked SPI-1. These findings provided the first evidence that strains deficient in SPI-1 could still cause intestinal disease, challenging the long-held assumption that SPI-1 is essential for the pathogenesis of salmonellosis in humans [26].

Subsequent comparative genomic and phenotypic analyses of 14 clinical *S.* Senftenberg isolates recovered from multiple outbreaks in Shenzhen and Shanghai between 2002 and 2011 identified two genetically distinct lineages, designated SC1 and SC2 [12]. SC2 clade included ST14 isolates associated with persistence in poultry that retained intact SPI-1 and SPI-2 loci and demonstrated a high capacity for host-cell invasion. In contrast, the SC1 clade comprised three sequence types (ST185, ST217 and ST1751) and included atypical non-H_2S-producing isolates carrying structural deletions in both SPI-1 and SPI-2 loci, which were associated with diminished invasiveness in vitro. Nevertheless, these isolates were capable of causing clinically significant disease in humans, highlighting the diversity of virulence strategies within this serovar. Comparative genomic analyses further identified additional genomic features potentially contributing to host colonization and persistence, including additional copies of the *shdA* gene in SPI-1-negative isolates. This heterogeneity illustrates why the biological and clinical significance of *S.* Senftenberg cannot be fully understood from conventional virulence markers alone and emphasizes the value of genomic approaches for detecting and characterizing atypical variants [12].

4. Conclusions

Although *S.* Senftenberg is not unique among *Salmonella* serovars, its remarkable capacity for survival, adaptation, together with its genetic and phenotypic diversity, makes it a valuable model for understanding bacterial adaptation in modern poultry production. Continued surveillance and integrated control strategies should therefore address not only the most prevalent serovars but also highly adapted lineages capable of persisting in production environments and entering the food chain. The continuous selective pressures imposed by control measures in intensive poultry production and food processing may favor the emergence and maintenance of increasingly adapted bacterial variants, while the capacity of bacteria to evolve may exceed the limits of existing surveillance and control strategies. In this context, the continued emergence of strains with novel combinations of persistence, stress tolerance, antimicrobial resistance, and virulence-associated traits remains a realistic possibility, with *S.* Senftenberg representing only one illustrative example.

The emergence of atypical variants that may escape conventional phenotypic identification further emphasizes the value of broader implementation of genomic methods and One Health surveillance integrating genomic data from food, environmental, animal, and clinical sources to better track pathogen evolution and transmission across ecological niches.

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